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OM nucleic - nucleic search, using sw model

Run on: September 17, 2002, 00:04:09 : Search time 3347.31 Seconds
(without alignments)
11588.820 Million cell updates/sec

Title: US-09-719-017A-2
Perfect score: 1793
Sequence: 1 gaattcccttgtagcaatla.....caattactcaatgcgcgcg 1793

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents_NA_Main:*

- 1: /cgn2_6/ptodata/2/pna/PCrus.COMB.seq:*
- 2: /cgn2_6/ptodata/2/pna/US06.COMB.seq:*
- 3: /cgn2_6/ptodata/2/pna/US07.COMB.seq:*
- 4: /cgn2_6/ptodata/2/pna/US080.COMB.seq:*
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- 27: /cgn2_6/ptodata/2/pna/US099E.COMB.seq:*
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- 29: /cgn2_6/ptodata/2/pna/US099G.COMB.seq:*
- 30: /cgn2_6/ptodata/2/pna/US099H.COMB.seq:*
- 31: /cgn2_6/ptodata/2/pna/US099I.COMB.seq:*
- 32: /cgn2_6/ptodata/2/pna/US099J.COMB.seq:*
- 33: /cgn2_6/ptodata/2/pna/US099K.COMB.seq:*
- 34: /cgn2_6/ptodata/2/pna/US099L.COMB.seq:*
- 35: /cgn2_6/ptodata/2/pna/US099M.COMB.seq:*
- 36: /cgn2_6/ptodata/2/pna/US099N.COMB.seq:*
- 37: /cgn2_6/ptodata/2/pna/US100.COMB.seq:*
- 38: /cgn2_6/ptodata/2/pna/US101.COMB.seq:*
- 39: /cgn2_6/ptodata/2/pna/US6000.COMB.seq:*
- 40: /cgn2_6/ptodata/2/pna/US6001.COMB.seq:*
- 41: /cgn2_6/ptodata/2/pna/US6002.COMB.seq:*
- 42: /cgn2_6/ptodata/2/pna/US6003.COMB.seq:*
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	Result No.	Score	Query Match	Length	DB ID	Description
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45:	2	401.6	22.4	7615	15	US-09-502-401-87
46:	3	401.6	22.4	7615	19	US-09-502-424-87
47:	4	401.6	22.4	7615	15	US-09-502-498-87
48:	5	401.6	22.4	7688	15	US-09-108-401-89
49:	6	401.6	22.4	7688	19	US-09-502-424-89
50:	7	401.6	22.4	7688	19	US-09-502-498-89
51:	8	401.6	22.4	7797	15	US-09-108-401-88
52:	9	401.6	22.4	7797	19	US-09-502-424-88
53:	10	401.6	22.4	7797	19	US-09-502-498-88
54:	11	369	20.6	7416	34	US-09-900-575-46
55:	12	336	18.7	5641	24	US-09-630-931A-13
56:	13	336	18.7	5620	24	US-09-630-931A-14
57:	14	336	18.7	5876	24	US-09-630-931A-11
58:	15	336	18.7	6043	24	US-09-630-929-9
59:	16	336	18.7	6071	24	US-09-630-931A-12
60:	17	332.8	18.6	4214	33	US-09-869-696-1
61:	18	332.8	18.6	4357	30	US-09-795-872-10
62:	19	332.8	18.6	5013	15	US-09-183-188A-5
63:	20	332.8	18.6	5013	15	US-09-183-188B-5
64:	21	332.8	18.6	5027	13	PCT-US98-27498-6
65:	22	332.8	18.6	5027	13	US-08-996-744-6
66:	23	332.8	18.6	5069	1	PCT-US98-27498-12
67:	24	332.8	18.6	5069	1	PCT-US98-27498-15
68:	25	332.8	18.6	5069	13	US-08-996-744-12
69:	26	332.8	18.6	5069	13	US-08-996-744-15
70:	27	332.8	18.6	5099	1	PCT-US98-27498-17
71:	28	332.8	18.6	5132	1	PCT-US98-27498-24
72:	29	332.8	18.6	5132	13	US-08-996-744-24
73:	30	332.8	18.6	5324	1	PCT-US98-27498-31
74:	31	332.8	18.6	5324	13	US-08-996-744-31

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	954.2	53.2	1071	31	US-09-806-876A-1
2	401.6	22.4	7615	15	US-09-502-401-87
3	401.6	22.4	7615	19	US-09-502-424-87
4	401.6	22.4	7615	15	US-09-502-498-87
5	401.6	22.4	7688	15	US-09-108-401-89
6	401.6	22.4	7688	19	US-09-502-424-89
7	401.6	22.4	7688	19	US-09-502-498-89
8	401.6	22.4	7797	15	US-09-108-401-88
9	401.6	22.4	7797	19	US-09-502-424-88
10	401.6	22.4	7797	19	US-09-502-498-88
11	369	20.6	7416	34	US-09-900-575-46
12	336	18.7	5641	24	US-09-630-931A-13
13	336	18.7	5620	24	US-09-630-931A-14
14	336	18.7	5876	24	US-09-630-931A-11
15	336	18.7	6043	24	US-09-630-929-9
16	336	18.7	6071	24	US-09-630-931A-12
17	332.8	18.6	4214	33	US-09-869-696-1
18	332.8	18.6	4357	30	US-09-795-872-10
19	332.8	18.6	5013	15	US-09-183-188A-5
20	332.8	18.6	5013	15	US-09-183-188B-5
21	332.8	18.6	5027	13	PCT-US98-27498-6
22	332.8	18.6	5027	13	US-08-996-744-6
23	332.8	18.6	5069	1	PCT-US98-27498-12
24	332.8	18.6	5069	1	PCT-US98-27498-15
25	332.8	18.6	5069	13	US-08-996-744-12
26	332.8	18.6	5069	13	US-08-996-744-15
27	332.8	18.6	5099	1	PCT-US98-27498-17
28	332.8	18.6	5132	1	PCT-US98-27498-24
29	332.8	18.6	5132	13	US-08-996-744-24
30	332.8	18.6	5324	1	PCT-US98-27498-31
31	332.8	18.6	5324	13	US-08-996-744-31

ALIGNMENTS

Query Match	53.2%;	Score 954.2;	DB 31;	Length 1071;
Best Local Similarity	93.2%;	Pred. No. 6.9e-250;		
Matches 998; Conservative	0;	Mismatches 73;	Indels 0;	Gaps 0;

[illegible]

Best Local Similarity 96.7%; Pred. No. 2.2e-98;
Matches 410; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY	1267	agagtcgaccttgcaagcagcagtcgaaagctcttggtctcccaactcgaccccatctgcgaactccagaag	1326
Db	318	agaattctgcctgcggcgagtaagcgcgctggtctcccaactcgaccccatctgcgaactccagaag	377
QY	1327	tgaacgcgcgtaaagccgaaatgtagtctgtaggtctctcccatctcgaaataaggaactgcc	1386
Db	378	tgaacgcgcgtaaagccgaaatgtagtctgtaggtctctcccatctcgaaataaggaactgcc	437
QY	1387	aggcacataaataaacaacgaaagctcagctcgaaagactcggtgccttcgtttacctgtgt	1446
Db	438	aggcacataaataaacaacgaaagctcagctcgaaagactcggtgccttcgtttacctgtgt	497
QY	1447	ttgtcggttgaaagcgtctctccgaaataagaaataatccgcggagtcgagatttgaacgttgcg	1506
Db	498	ttgtcggttgaaagcgtctctccgaaataagaaataatccgcggagtcgagatttgaacgttgcg	557
QY	1507	aagcaaacgcgcgcgagaggttgtagcgagcagaagacgcgccgcctaaactcgcgaagcatcaaat	1566
Db	558	aagcaaacgcgcgcgagaggttgtagcgagcagaagacgcgccgcctaaactcgcgaagcatcaaat	617
QY	1567	aagcagaagaagcgcaccttgaaagatgagccttttgcgtttctcaaacctctccgtgcgtc	1626
Db	618	aagcagaagaagaagcgcaccttgaaagatgagccttttgcgtttctcaaacctctccgtgcgtc	677
QY	1627	atactctcaagcgcacctccccacagataagcgttaaaactagcctctgttttgatcagaagaa	1686
Db	678	atactctcaagcgcacctccccacagataagcgttaaaactagcctctgttttgatcagaagaa	737
QY	1687	gcacg 1690	
Db	738	gcacg 741	

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RESULT 3
US-09-502-424-87
: Sequence 87, Application US/09502424
: GENERAL INFORMATION:
: APPLICANT: Killian, Andrzej
: APPLICANT: Bowtell, David
: TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND USE
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: 190106.407
: CURRENT APPLICATION NUMBER: US/09/502,424
: CURRENT FILING DATE: 2000-02-11
: PRIORITY APPLICATION NUMBER: US 09/108,401
: PRIORITY FILING DATE: 1998-06-30
: NUMBER OF SEQ ID NOS: 155
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 87
: LENGTH: 7615
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Human Telomerase Clone with Exon Beta Spliced Out
US-09-502-424-87

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Query Match	22.4%	Score 401.6;	DB 19;	Length 7615;
Best Local Similarity	96.7%;	Pred. No. 2.2e-98;		
Matches 410;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0;

[illegible][illegible]

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RESULT 4
: Sequence 87, Application US/09502498
: GENERAL INFORMATION:
: APPLICANT: Killian, Andrzej
: APPLICANT: Bowtell, David
: TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES
: TITLE OF INVENTION: THERCOP
: FILE REFERENCE: 190106.407
: CURRENT APPLICATION NUMBER: US/09/502,498
: CURRENT FILING DATE: 2000-02-11
: PRIOR APPLICATION NUMBER: US 09/108,401
: PRIOR FILING DATE: 1998-06-30
: NUMBER OF SEQ. ID NOS: 155
: SOFTWARE: Patencin Ver. 2.0
: SEQ ID NO 87
: LENGTH: 7615
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Human Telomerase Clone with Exon Beta Spliced Out
US-09-502-498-87

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Query Match	22.4%;	Score 401.6;	DB 19;	Length 7615;
Best Local Similarity	96.7%;	Pred. No. 2.2e-98;		
Matches 410; Conservative	0;	Mismatches 14;	Indels 0;	Gaps 0;

QY	1267	agagtcgacgctcgcaagctgcaacgcttggcttcccactgaccccaatgcggaatccagaag	1326
Db	318	agaatttccttcgcygcgcatgacgcygtgttcccaactgaccccaatgcygcaatcaagaag	377
QY	1327	tgaaacgcgcgtacgcgcgatgtagtctgtggggctcccccatacgagaaatgaagaactgcc	1386
Db	378	tgaaacgcgcgtacgcgcgatgtagtctgtggggctcccccatacgagaaatgaagaactgcc	437
QY	1387	aggctcaataataaacggaagcgtcactgacgaaagactgagccttctgctttatctgtgtc	1446
Db	438	aggctcaataataaacggaagcgtcactgacgaaagactgagccttctgctttatctgtgtc	497
QY	1447	tgtcgctggaacgcgtctctcctgtagtgaagacaatcccgccggagcggaaatttgaacgttcg	1506
Db	498	tgtcgctggaacgcgtctctcctgtagtgaagacaatcccgccggagcggaaatttgaacgttcg	557
QY	1507	aagcaacgccccggaggggtgtgcgagcaagaacgccgcataaactgcgaagcatcaaat	1566
Db	558	aagcaacgccccggaggggtgtgcgagcaagaacgccgcataaactgcgaagcatcaaat	617
QY	1567	aagcgaagggccatccttaacgaatgagccttcttgctttctacaacaactctccgtgctc	1626

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Db 618 aagcagaagccatctcgaagatgagccttctgcttcttaaaactctctgctgc 677
Qy 1627 atatcacaagccatccccccacagatacgttaactagcctctgttttgcacaga 1686
Db 678 atatcacaagccatccccccacagatacgttaactagcctctgttttgcacaga 737
Qy 1687 gcag 1690
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RESULT 5
; Sequence 89, Application US/09108401
; GENERAL INFORMATION:
; APPLICANT: Killian, Andrzej
; APPLICANT: Bowtell, David
; TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES
; FILE REFERENCE: 190106.407
; CURRENT APPLICATION NUMBER: US/09/108,401
; CURRENT FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 89
; LENGTH: 7688
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Telomerase Clone with exon Alpha Spliced Out
US-09-108-401-89

Query Match 22.4%; Score 401.6; DB 15; Length 7688;
Best Local Similarity 96.7%; Pred. No. 2.2e-98;
Matches 410; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1267 agagtcgacctgcagcagcagcagccttggtccacatgaccccatgcggaactcagaag 1326
Db 318 agaattgctctgagcagatagcgcgtggtccacatgaccccatgcggaactcagaag 377
Qy 1327 tgaacgcgtagcgcagatgtagtctgtggtctcccatgagagtagggaactgcc 1386
Db 378 tgaacgcgtagcgcagatgtagtctgtggtctcccatgagagtagggaactgcc 437
Qy 1387 aagcacaataaagaagaagctcagtcgaagacttgagccttctgtttatctgtgt 1446
Db 438 aagcacaataaagaagaagctcagtcgaagacttgagccttctgtttatctgtgt 497
Qy 1447 tctgcgtgaacgctctcctgaatagacaataatccgcggagcagatttgaacgttgcg 1506
Db 498 tctgcgtgaacgctctcctgaatagacaataatccgcggagcagatttgaacgttgcg 557
Qy 1507 aagcaacgcccggaggtggtgcgcagagacgcgcgcataaactgcagcgcataaatt 1566
Db 558 aagcaacgcccggaggtggtgcgcagagacgcgcgcataaactgcagcgcataaatt 617
Qy 1567 aagcagaagccatctcgaagatgagccttctgtcttcttaaaactctctgtcgtc 1626
Db 618 aagcagaagccatctcgaagatgagccttctgtcttcttaaaactctctgtcgtc 677
Qy 1627 atatcacaagccatccccccacagatacgttaactagcctctgttttgcacaga 1686
Db 678 atatcacaagccatccccccacagatacgttaactagcctctgttttgcacaga 737
Qy 1687 gcag 1690
|||||
Db 738 gcag 741

RESULT 6
US-09-502-424-89
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; Sequence 89, Application US/09502424
; GENERAL INFORMATION:
; APPLICANT: Killian, Andrzej
; APPLICANT: Bowtell, David
; TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES
; FILE REFERENCE: 190106.407
; CURRENT APPLICATION NUMBER: US/09/502,424
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 09/108,401
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 89
; LENGTH: 7688
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Telomerase Clone with exon Alpha Spliced Out
US-09-502-424-89

Query Match 22.4%; Score 401.6; DB 19; Length 7688;
Best Local Similarity 96.7%; Pred. No. 2.2e-98;
Matches 410; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1267 agagtcgacctgcagcagcagcagccttggtccacatgaccccatgcggaactcagaag 1326
Db 318 agaattgctctgagcagatagcgcgtggtccacatgaccccatgcggaactcagaag 377
Qy 1327 tgaacgcgtagcgcagatgtagtctgtggtctcccatgagagtagggaactgcc 1386
Db 378 tgaacgcgtagcgcagatgtagtctgtggtctcccatgagagtagggaactgcc 437
Qy 1387 aagcacaataaagaagaagctcagtcgaagacttgagccttctgtttatctgtgt 1446
Db 438 aagcacaataaagaagaagctcagtcgaagacttgagccttctgtttatctgtgt 497
Qy 1447 tctgcgtgaacgctctcctgaatagacaataatccgcggagcagatttgaacgttgcg 1506
Db 498 tctgcgtgaacgctctcctgaatagacaataatccgcggagcagatttgaacgttgcg 557
Qy 1507 aagcaacgcccggaggtggtgcgcagagacgcgcgcataaactgcagcgcataaatt 1566
Db 558 aagcaacgcccggaggtggtgcgcagagacgcgcgcataaactgcagcgcataaatt 617
Qy 1567 aagcagaagccatctcgaagatgagccttctgtcttcttaaaactctctgtcgtc 1626
Db 618 aagcagaagccatctcgaagatgagccttctgtcttcttaaaactctctgtcgtc 677
Qy 1627 atatcacaagccatccccccacagatacgttaactagcctctgttttgcacaga 1686
Db 678 atatcacaagccatccccccacagatacgttaactagcctctgttttgcacaga 737
Qy 1687 gcag 1690
|||||
Db 738 gcag 741

RESULT 7
US-09-502-498-89
; Sequence 89, Application US/09502498
; GENERAL INFORMATION:
; APPLICANT: Killian, Andrzej
; APPLICANT: Bowtell, David
; TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES
; FILE REFERENCE: 190106.407
; CURRENT APPLICATION NUMBER: US/09/502,498
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 09/108,401
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 155
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Query Match	22.4%	Score 401.6;	DB 15;	Length 7797;
Best Local Similarity	96.7%;	Pred. No. 2.2e-98;		
Matches 410; Conservative	0;	Mismatches 14;	Indels 0;	Gaps 0

OY	125	agagatcgagacgtcgccagcagatgcataagctttggtgtccaccacttaccacccatgcccgaactcaagaag	1326
Db	318	agaatttcgctcgtgcgcgcagctagcgcgttgggtccaccctgacccccaatgcgaactcaagaag	377
OY	1327	tgaaacgcgcgttagcgcgcgatgctgtagtctgttgggtgtctcccatgcgaagaatgaggaacttcc	1366
Db	378	tgaaacgcgcgttagcgcgcgatgctgtagtctgttgggtgtctcccatgcgaagaatgaggaacttcc	437
OY	1387	aggcacataataaaccgaagagctcagctcgaagaagcttggcctttcgttttatctctgtgt	1448
Db	438	agagatcaataataaaccgaagagctcagctcgaagaagcttggcctttcgttttatctctgtgt	497

FILE REFERENCE: ELITRA.006A
CURRENT APPLICATION NUMBER: US/09/630.931A
CURRENT FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/159,221
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 5641
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pJMF3
US-09-630-931A-13

Query Match 18.7%, Score 336; DB 24; Length 5641;
Best Local Similarity 100.0%; Pred. No. 1.8e-80;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1311 atgccgaactcagaagtgaacgcccgtagcgcgagtgtagtgggtctcccatg 1370
|||
Db 1441 atgccgaactcagaagtgaacgcccgtagcgcgagtgtagtgggtctcccatg 1500
OY 1371 agagtgaaggaaactgcgaagcatcaataaagaaggctcagtcgaagactggcctt 1430
|||
Db 1501 agagtgaaggaaactgcgaagcatcaataaagaaggctcagtcgaagactggcctt 1560
OY 1431 tcgtttatctgtgtgttgcgtgtagaagctctcctgagtagaacaatccgcggagc 1490
|||
Db 1561 tcgtttatctgtgtgttgcgtgtagaagctctcctgagtagaacaatccgcggagc 1620
OY 1491 ggatttgaacgttgcgaagcaagcccgaggtggtgcggcgagagcccgccataac 1550
|||
Db 1621 ggatttgaacgttgcgaagcaagcccgaggtggtgcggcgagagcccgccataac 1680
OY 1551 tgcagagcatcaaatlaagcagaagggccatcctgacggatggccttttgcgtttctaca 1610
|||
Db 1681 tgcagagcatcaaatlaagcagaagggccatcctgacggatggccttttgcgtttctaca 1740
OY 1611 aactcttcctgtcgtcatatctacaagccatcccc 1646
|||
Db 1741 aactcttcctgtcgtcatatctacaagccatcccc 1776

RESULT 13
US-09-630-931A-14
Sequence 14, Application US/09630931A
GENERAL INFORMATION:
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: CHITOBIASE AS A REPORTER ENZYME
FILE REFERENCE: ELITRA.006A
CURRENT APPLICATION NUMBER: US/09/630.931A
CURRENT FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/159,221
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 5670
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pJMF4
US-09-630-931A-14

Query Match 18.7%, Score 336; DB 24; Length 5670;
Best Local Similarity 100.0%; Pred. No. 1.8e-80;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1311 atgccgaactcagaagtgaacgcccgtagcgcgagtgtagtgggtctcccatg 1370
|||

Db 1441 atgccgaactcagaagtgaacgcccgtagcgcgagtgtagtgggtctcccatg 1500
OY 1371 agagtgaaggaaactgcgaagcatcaataaagaaggctcagtcgaagactggcctt 1430
|||
Db 1501 agagtgaaggaaactgcgaagcatcaataaagaaggctcagtcgaagactggcctt 1560
OY 1431 tcgtttatctgtgtgttgcgtgtagaagctctcctgagtagaacaatccgcggagc 1490
|||
Db 1561 tcgtttatctgtgtgttgcgtgtagaagctctcctgagtagaacaatccgcggagc 1620
OY 1491 ggatttgaacgttgcgaagcaagcccgaggtggtgcggcgagagcccgccataac 1550
|||
Db 1621 ggatttgaacgttgcgaagcaagcccgaggtggtgcggcgagagcccgccataac 1680
OY 1551 tgcagagcatcaaatlaagcagaagggccatcctgacggatggccttttgcgtttctaca 1610
|||
Db 1681 tgcagagcatcaaatlaagcagaagggccatcctgacggatggccttttgcgtttctaca 1740
OY 1611 aactcttcctgtcgtcatatctacaagccatcccc 1646
|||
Db 1741 aactcttcctgtcgtcatatctacaagccatcccc 1776

RESULT 14
US-09-630-931A-11
Sequence 11, Application US/09630931A
GENERAL INFORMATION:
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: CHITOBIASE AS A REPORTER ENZYME
FILE REFERENCE: ELITRA.006A
CURRENT APPLICATION NUMBER: US/09/630.931A
CURRENT FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/159,221
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 5826
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pDK9
US-09-630-931A-11

Query Match 18.7%, Score 336; DB 24; Length 5826;
Best Local Similarity 100.0%; Pred. No. 1.8e-80;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1311 atgccgaactcagaagtgaacgcccgtagcgcgagtgtagtgggtctcccatg 1370
|||
Db 1441 atgccgaactcagaagtgaacgcccgtagcgcgagtgtagtgggtctcccatg 1500
OY 1371 agagtgaaggaaactgcgaagcatcaataaagaaggctcagtcgaagactggcctt 1430
|||
Db 1501 agagtgaaggaaactgcgaagcatcaataaagaaggctcagtcgaagactggcctt 1560
OY 1431 tcgtttatctgtgtgttgcgtgtagaagctctcctgagtagaacaatccgcggagc 1490
|||
Db 1561 tcgtttatctgtgtgttgcgtgtagaagctctcctgagtagaacaatccgcggagc 1620
OY 1491 ggatttgaacgttgcgaagcaagcccgaggtggtgcggcgagagcccgccataac 1550
|||
Db 1621 ggatttgaacgttgcgaagcaagcccgaggtggtgcggcgagagcccgccataac 1680
OY 1551 tgcagagcatcaaatlaagcagaagggccatcctgacggatggccttttgcgtttctaca 1610
|||
Db 1681 tgcagagcatcaaatlaagcagaagggccatcctgacggatggccttttgcgtttctaca 1740
OY 1611 aactcttcctgtcgtcatatctacaagccatcccc 1646
|||
Db 1741 aactcttcctgtcgtcatatctacaagccatcccc 1776

```
RESULT 15
US-09-630-929-4
; Sequence 4, Application US/09630929
; GENERAL INFORMATION:
; APPLICANT: Judith W. Zyskind
; TITLE OF INVENTION: USE OF ECTOENZYMES AND SECRETED ENZYMES
; TITLE OF INVENTION: TO MONITOR CELLULAR PROLIFERATION
; FILE REFERENCE: ELITRA.012A
; CURRENT APPLICATION NUMBER: US/09/630,929
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 6043
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Engineered E. coli plasmid pUFK4 with V. harvey1
; OTHER INFORMATION: sequences inserted
US-09-630-929-4
```

```
Query Match 18.7%; Score 336; DB 24; Length 6043;
Best Local Similarity 100.0%; Pred. NO. 1.8e-80;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1311 atgcccgaactcgaagtggaacgcgtaagccgagatgtagtctggtgtccccaatgcg 1370
   |||
DB 1441 atgcccgaactcgaagtggaacgcgtaagccgagatgtagtctggtgtccccaatgcg 1500

QY 1371 agagtagggaaactcgaagcacaataaagcgaagctcagtcgaagaacttggtcctt 1430
   |||
DB 1501 agagtagggaaactcgaagcacaataaagcgaagctcagtcgaagaacttggtcctt 1560

QY 1431 tcgtttatctgtctgttcggtgaacgctcctcctgaagtagaacaatccgcgggaagc 1490
   |||
DB 1561 tcgtttatctgtctgttcggtgaacgctcctcctgaagtagaacaatccgcgggaagc 1620

QY 1491 ggaattgaaagctgcgaagcaacgcccgaaggttgccgagcagaagcgcgcacataaac 1550
   |||
DB 1621 ggaattgaaagctgcgaagcaacgcccgaaggttgccgagcagaagcgcgcacataaac 1680

QY 1551 tgcaggagcacaataaagcagaagcgaatcctgaagcgaatggtcctttggtttctaca 1610
   |||
DB 1681 tgcaggagcacaataaagcagaagcgaatcctgaagcgaatggtcctttggtttctaca 1740

QY 1611 aactctcctgcgtcatalctacaagcattccccc 1646
   |||
DB 1741 aactctcctgcgtcatalctacaagcattccccc 1776
```

Search completed: September 17, 2002, 02:38:37
Job time: 9268 sec